

Steps to unravel the sequence of the resistance locus *Ren3* against powdery mildew (*Erysiphe necator*) originally identified in the grapevine cultivar 'Regent'

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Powdery mildew is one of the most devastating diseases of grapevine (*Vitis vinifera* L). The disease is caused by *Erysiphe necator* Schw. (syn. *Uncinula necator* (Schw.) Burr, anamorph *Oidium tuckeri* Berk.), an ascomycete fungus, which was introduced from North America to Europe in 1845. The traditional European cultivars are highly susceptible to the fungus and still today huge amounts of fungicides are necessary to defeat the pathogen.

Many North American *Vitis* species developed resistance against *Erysiphe necator* due to co-evolution of host and pathogen. This process promoted the development of a genetic locus called *Ren3*, which was characterized by Fischer et al. (2004) in the cultivar 'Regent'. Later Dudenhöffer and Zyprian (2012) showed that several genes are located within this region, which show great similarity to genes known to mediate resistances in other plants.

Recent work in this project focuses on unraveling the complete sequence of the *Ren3* locus via screening of 22.000 BAC clones. In a 4D approach a 'Regent' BAC library was screened for BACs located within the locus. The gaps left in the sequence will be closed by re-sequencing of previously identified BAC clones and amplicon sequencing.

The obtained sequences permit searching for open reading frames which contain functional domain structures already known from identified resistance genes. Subsequently an expression analysis will be performed.

Some of these genes shall be cloned into a binary expression vector and checked for functionality upon transformation of susceptible grapevine cultivars with *Agrobacterium tumefaciens*.

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